Amendments to the Specification:

Please replace the paragraph number [00054] (spanning pages 12-13) of the as-filed specification, with the following rewritten paragraph:

-- The expression of the TM protein was analyzed by 4-20% gradient SDS-PAGE gel electrophoresis and visualized by Western blot analysis using a mouse monoclonal antibody to human thrombomodulin. The target protein was expressed as a N-terminal Dsba enzyme fusion to a leader sequence containing an *Enterokinase* cleavage site, hexahistidine, and S-tags (protein **TM_A**). S-Tag Rapid Assay was used to quantify protein concentration and therefore expression yield, which averaged 17 mg/L of cell culture. **TM_A** was purified from the cell pellet by using immobilized metal-affinity chromatography on ~~TALON~~ TALON™ resin (Clontech Laboratories, Inc.) under native conditions using an imidazole gradient for elution of the target polypeptide. The cells were first harvested by centrifugation at 4 °C at 10,000g for 30 min and resuspended in 25 mL of lysis buffer (300 mM NaCl, 50 mM NaH_2PO_4, 10% glycerol, 1 mg/mL lysozyme, 10 μg/mL PMSF, pH 8). After incubation on ice for 30min, the cell lysate was clarified by centrifugation at 10,000g for 20 min. The soluble extract was then loaded onto a column containing ~~TALON~~ TALON™ metal affinity resin (25 mL), which had been preequilibrated with lysis buffer. The weakly binding proteins were removed by rinsing the column with 125 mL wash buffer (300 mM NaCl, 50 mM NaH_2PO_4, 10% glycerol, 20mM imidazole, pH 8). **TM_A** was eluted by the addition of 50 mL of elution buffer (300 mM NaCl, 50 mM NaH_2PO_4, 10% glycerol, 250mM imidazole, pH 8). The chromatographic fractions were analyzed by 4-20% gradient SDS-PAGE gel electrophoresis and visualized by Western blot analysis using mouse monoclonal antibody to human thrombomodulin. The nitrocellulose membrane was developed using the ECL plus Western blotting detection kit (Amersham Biosciences, UK). *Enterokinase* cleavage removed the fusion tag and generated the target protein (**TM_B**). N-terminal sequencing, amino acid compositional and mass analysis (SELDI-TOF) confirmed the integrity of **TM_B**: (Mass detected (m/z): 16,545.2 D (calculated 16,540.1 D)). --